510(k) Summary

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BD MAX™ Enteric Bacterial Panel

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Device:

510(k) Number:	K140111
Trade Name:	BD MAX™ Enteric Bacterial Panel
Common Name:	Gastrointestinal pathogen panel multiplex nucleic acid-based assay system
Classification:	Class II
Regulation Number:	866.3990
Product Code:	PCI, PCH, OOI
Panel:	Microbiology (83)
Predicate Device:	Gen-Probe Prodesse, Inc. ProGastro SSCS Assay
Predicate 510(k) Numbers:	K123274

Intended Use

The BD MAX™ Enteric Bacterial Panel performed on the BD MAX™ System is an automated *in vitro* diagnostic test for the direct qualitative detection and differentiation of enteric bacterial pathogens. The BD MAX Enteric Bacterial Panel detects nucleic acids from:

- *Salmonella* spp.
- *Campylobacter* spp. (*jejuni* and *coli*)
- *Shigella* spp. / Enteroinvasive *E. coli* (EIEC)
- Shiga toxin 1 (*stx*1) / Shiga toxin 2 (*stx*2) genes (found in Shiga toxin-producing *E. coli* [STEC]) as well as *Shigella dysenteriae*, which can possess a Shiga toxin gene (*stx*) that is identical to the *stx*1 gene of STEC.

Testing is performed on unpreserved soft to diarrheal stool specimens or Cary-Blair preserved stool specimens from symptomatic patients with suspected acute gastroenteritis, enteritis or colitis. The test is performed directly on the specimen, utilizing real-time polymerase chain reaction (PCR) for the amplification of *SpaO*, a *Campylobacter* specific *tuf* gene sequence, *ipaH* and *stx*1/*stx*2. The test utilizes fluorogenic sequence-specific hybridization probes for detection of the amplified DNA.

This test is intended for use, in conjunction with clinical presentation, laboratory findings, and epidemiological information, as an aid in the differential diagnosis of *Salmonella*, *Shigella*/EIEC, *Campylobacter* and Shiga toxin-producing *E. coli* (STEC) infections. Results of this test should not be used as the sole basis for diagnosis, treatment, or other patient management decisions. Positive results do not rule out co-infection with other organisms that are not detected by this test, and may not be the sole or definitive cause of patient illness. Negative results in the setting of clinical illness compatible with gastroenteritis may be due to infection by pathogens that are not detected by this test or non-infectious causes such as ulcerative colitis, irritable bowel syndrome, or Crohn's disease.

Special Conditions for Use Statement: For prescription use

Special Instrument Requirements: BD MAX™ System

Device Description

The BD MAX™ System and the BD MAX™ Enteric Bacterial Panel are comprised of an instrument with associated hardware and accessories, disposable microfluidic cartridges, master mixes, unitized reagent strips, extraction reagents, and sample buffer tubes. The instrument automates sample preparation including target lysis, DNA extraction and concentration, reagent rehydration, and target nucleic acid amplification and detection using real-time PCR. The assay includes a Sample Processing Control (SPC) that is present in the Extraction Tube. The SPC monitors DNA extraction steps, thermal cycling steps, reagent integrity and the presence of inhibitory substances. The BD MAX™ System software automatically interprets test results. A test result may be called as POS, NEG or UNR for each of the assay's targets, based on the amplification status of the target and of the Sample Processing Control. IND (Indeterminate) or INC (Incomplete) results are due to BD MAX™ System failure.

Test Principle

The BD MAX™ Enteric Bacterial Panel performed on the BD MAX™ System is an automated *in vitro* diagnostic test for the direct, qualitative detection of enteric bacterial pathogens responsible for gastreoenteritis due to *Salmonella* spp., *Campylobacter* spp. (*jejuni* and *coli*), *Shigella* spp. / Enteroinvasive *E. coli* (EIEC), and Shiga toxin-producing E. coli (STEC) as well as *Shigella dysenteriae*, which can possess a Shiga toxin gene (*stx*) that is identical to the *stx*1 gene of STEC. The BD MAX Enteric Bacterial Panel detects target DNA from unpreserved soft to diarrheal stool specimens or Cary-Blair preserved stool specimens from symptomatic patients with suspected acute gastroenteritis, enteritis or colitis.

A stool specimen is collected and transported to the laboratory in a dry, clean container (for unpreserved specimens) or in Cary-Blair transport media. The specimen is vortexed

for 15 seconds and then a 10 µL loop is used to inoculate a BD MAX™ Enteric Bacterial Panel Sample Buffer Tube. The Sample Buffer Tube is closed with a septum cap and vortexed. A worklist is created and the Sample Buffer Tube, the BD MAX™ Enteric Bacterial Panel unitized reagent strip (URS) and the BD MAX™ PCR Cartridge are loaded onto the BD MAX™ System.

Following enzymatic cell lysis, the released nucleic acids are captured on magnetic beads. The beads, with the bound nucleic acids, are washed using Wash Buffer and the nucleic acids are eluted by heat in Elution Buffer. Eluted DNA is neutralized using Neutralization Buffer and transferred to a Master Mix to rehydrate PCR reagents. After reconstitution, the BD MAX™ System dispenses a fixed volume of PCR-ready solution containing extracted nucleic acids into the BD MAX™ PCR Cartridge. Microvalves in the BD MAX™ PCR Cartridge are sealed by the system prior to initiating PCR to contain the amplification mixture, thus preventing evaporation and contamination.

The amplified DNA targets are detected using hydrolysis (TaqMan®) probes, labeled at one end with a fluorescent reporter dye (fluorophore) and at the other end with a quencher moiety. Probes labeled with different fluorophores are used to detect amplicons for enteric bacterial targets (*Campylobacter* specific *tuf* gene sequence variants, the *SpaO* gene for specific detection of *Salmonella* spp., the *ipaH* gene for specific detection of *Shigella* spp. / Enteroinvasive *E. coli* (EIEC), the *stx*1 & *stx*2 genes associated with production of Shiga toxins in STEC and *S. dysenteriae)* and the SPC in five different optical channels of the BD MAX System. When the probes are in their native state, the fluorescence of the fluorophore is quenched due to its proximity to the quencher. However, in the presence of target DNA, the probes hybridize to their complementary sequences and are hydrolyzed by the 5'-3' exonuclease activity of the DNA polymerase as it synthesizes the nascent strand along the DNA template. As a result, the fluorophores are separated from the quencher molecules and fluorescence is emitted. The amount of fluorescence detected in the optical channels used for the BD MAX™ Enteric Bacterial Panel is directly proportional to the quantity of the corresponding probe that is hydrolyzed. The BD MAX™ System measures these signals at the end of each amplification cycle, and interprets the data to provide a result.

Substantial Equivalence

Table 1 shows the similarities and differences between the BD MAX™ Enteric Bacterial Panel and the predicate device.

Table 1: Substantial Equivalence[1] Information

ITEM	BD MAX™ Enteric Bacterial Panel	Hologic® Prodesse® ProGastro™ SSCS (K123274)
Intended Use	The BD MAX™ Enteric Bacterial Panel performed on the BD MAX™ System is an automated *in vitro* diagnostic test for the direct qualitative detection and differentiation of enteric bacterial pathogens. The BD MAX Enteric Bacterial Panel detects nucleic acids from: • *Salmonella* spp. • *Campylobacter* spp. (*jejuni* and *coli*) • *Shigella* spp. / Enteroinvasive *E. coli* (EIEC) • Shiga toxin 1 (*stx*1) / Shiga toxin 2 (*stx*2) genes (found in Shiga toxin-producing *E. coli* [STEC]) as well as *Shigella dysenteriae*, which can possess a Shiga toxin gene (*stx*) that is identical to the *stx*1 gene of STEC. Testing is performed on unpreserved soft to diarrheal stool specimens or Cary-Blair preserved stool specimens from symptomatic patients with suspected acute gastroenteritis, enteritis or colitis. The test is performed directly on the specimen, utilizing real-time polymerase chain reaction (PCR) for the amplification of *SpaO*, a *Campylobacter* specific *tuf* gene sequence, *ipaH* and *stx*1/*stx*2. The test utilizes fluorogenic sequence-specific hybridization probes for detection of the amplified DNA. This test is intended for use, in conjunction with clinical presentation, laboratory findings, and epidemiological information, as an aid in the differential diagnosis of *Salmonella*, *Shigella*/EIEC, *Campylobacter* and Shiga toxin-producing *E. coli* (STEC) infections. Results of this test should not be	The Prodesse® ProGastro SSCS Assay is a multiplex real time PCR in vitro diagnostic test for the qualitative detection and differentiation of *Salmonella*, *Shigella*, and *Campylobacter* (*C. jejuni* and *C. coli* only, undifferentiated) nucleic acids and Shiga Toxin 1 (*stx1*) and Shiga Toxin 2 (*stx2*) genes. Shiga toxin producing *E. coli* (STEC) typically harbor one or both genes that encode for Shiga Toxins 1 and 2. Nucleic acids are isolated and purified from preserved stool specimens obtained from symptomatic patients exhibiting signs and symptoms of gastroenteritis. This test is intended for use, in conjunction with clinical presentation and epidemiological risk factors, as an aid in the differential diagnosis of *Salmonella*, *Shigella*, *Campylobacter jejuni/Campylobacter coli*, and STEC infections in humans. The results of this test should not be used as the sole basis for diagnosis, treatment, or other patient management decisions. Positive results do not rule out co-infection with other organisms that are not detected by this test, and may not be the sole or definitive cause of patient illness. Negative ProGastro SSCS Assay results in the setting of clinical illness compatible with gastroenteritis may be due to infection by pathogens

[1] The term "substantial equivalence" as used in this 510(k) notification is limited to the definition of substantial equivalence as found in the Federal Food, Drug and Cosmetic Act, as amended and as applied under 21 CFR 807, Subpart E under which a device can be marketed without pre-market approval or reclassification. A determination of substantial equivalency under this notification is not intended to have any bearing whatsoever on the resolution of patent infringement suits or any other patent matters. No statements related to, or in support of substantial equivalence herein shall be construed as an admission against interest under the US Patent Laws or their application by the courts.

ITEM	BD MAX™ Enteric Bacterial Panel	Hologic® Prodesse® ProGastro™ SSCS (K123274)
	used as the sole basis for diagnosis, treatment, or other patient management decisions. Positive results do not rule out co-infection with other organisms that are not detected by this test, and may not be the sole or definitive cause of patient illness. Negative results in the setting of clinical illness compatible with gastroenteritis may be due to infection by pathogens that are not detected by this test or non-infectious causes such as ulcerative colitis, irritable bowel syndrome, or Crohn's disease.	that are not detected by this test or non-infectious causes such as ulcerative colitis, irritable bowel syndrome, or Crohn's disease.
Specimen type	Unpreserved and Cary-Blair preserved stool.	Stool in Cary-Blair preserved or Para-Pak® C&S transport medium.
Assay Format	Amplification: PCR Detection: fluorogenic target-specific hybridization.	Same
Mode of Detection for *Campylobacter*	Presence of *tuf* gene specific for *Campylobacter*.	Presence of *glyA* gene specific for *Campylobacter jejuni* and *cadF* gene specific for *C. coli*.
Mode of Detection for *Salmonella*	Presence of *SpaO* gene specific for *Salmonella*.	Presence of *orgC* gene specific for *Salmonella*.
Mode of Detection for *Shigella*	Presence of *ipaH* gene specific for *Shigella*/EIEC.	Presence of *ipaH* gene specific for *Shigella*.
Mode of Detection for Shiga toxins	Presence of *stx*1 and *stx*2 genes specific to Shiga toxin-producing organisms.	Presence of *stx*1 and *stx*2 genes specific to Shiga toxin-producing organisms.
Interpretation of Test Results	Automated (BD MAX™ System diagnostic software)	Automated (Cepheid SmartCycler® II)
Analysis Platform	BD MAX™ System	Cepheid SmartCycler® II
PCR Sample Preparation	Automated by the BD MAX™ System	bioMérieux NucliSENS® easyMAG®
Detection Probes	TaqMan® Probe	TaqMan® Probe
Assay Controls	Sample Processing Control (SPC)	Internal Control

Analytical Performance

Precision

Within-laboratory precision was evaluated for the BD MAX™ Enteric Bacterial Panel at one (1) site. The Precision panel consisted of 4 sample categories near the LoD. Each specimen contained negative stool matrix. Target strains were tested as follows:

- For moderate positives (MP): overall correct percentage of approximately 100% with 95% CI
- For low positives (LP): overall correct percentage of approximately 95% with 95% CI
- For true negatives (TN): overall correct percentage of approximately 100% with 95% CI
- For high negatives (HN): overall correct percentage between 20 and 80%

Testing was performed in triplicate, over 12 days, with 2 runs per day, by 2 different technologists. Precision study results are summarized below in **Table 2**.

Table 2: Within-laboratory Precision Testing

Target	Level	Correct	Total	% Correct
Shiga toxins	TN[1]	72	72	100.00%
	HN[1]	20	72	27.78%
	LP	71	72	98.61%
	MP	72	72	100.00%
Campylobacter	TN	72	72	100.00%
	HN	39	72	54.17%
	LP	72	72	100.00%
	MP	71	72	98.61%
Shigella	TN	72	72	100.00%
	HN	22	72	30.56%
	LP	71	72	98.61%
	MP	71	72	98.61%
Salmonella	TN	72	72	100.00%
	HN	18	72	25.00%
	LP	72	72	100.00%
	MP	72	72	100.00%

[1] For the True Negative (TN) and High Negative (HN) categories, the expected assay result was deemed to be negative. Therefore, percent agreement was calculated for negative results.

Reproducibility

For the Site-to-Site reproducibility study, three (3) clinical sites were provided with a total of ten (10) panels, each consisting of 12 tubes. The panels used were the same as described under the Precision heading, above. Each site was asked to perform the study on five (5) distinct days (consecutive or not), wherein each day, two (2) panels were tested, one (1) for each of two (2) technologists.

The overall Site-to-Site Reproducibility percent agreement was 100% for the TN category for all targets, and ranged from 41.1% to 77.8%, 96.7% to 100% and 98.9% to 100% for the HN, LP and MP categories, respectively (**Table 3**). The qualitative and

quantitative reproducibility across sites and by target is presented below in **Tables 4** through **10**. Ct.Score is an internal criterion used to determine final assay results and was selected as an additional means of assessing assay reproducibility. Overall mean Ct.Score values with variance components (SD and %CV) are shown in Tables **4**, **6**, **8** and **10**.

Table 3: Site-to-Site Reproducibility Study Results using one lot of the BD MAX Enteric Bacterial Panel

Category	*Campylobacter* (*coli* and *jejuni*) [n], (95% CI)	*Salmonella* spp. [n], (95% CI)	*Shigella* spp. [n], (95% CI)	Shiga toxins (*stx*1 and *stx*2) [n], (95% CI)
TN*	100.0%, [90/90], 95.9%, 100.0%)	100.0%, [90/90], (95.9%, 100.0%)	100.0%, [90/90], (95.9%, 100.0%)	100.0%, [90/90], (95.9%, 100.0%)
HN*	77.8%, [70/90], (68.2%, 85.1%)	44.4%, [40/90], (34.6%, 54.7%)	41.1%, [37/90], (31.5%, 51.4%)	50.0%, [45/90], (39.9%, 60.1%)
LP	100.0%, [90/90], (95.9%, 100.0%)	96.7%, [87/90], (90.7%, 98.9%)	97.8%, [88/90], (92.3%, 99.4%)	100.0%, [90/90], (95.9%, 100.0%)
MP	100.0%, [90/90], (95.9%, 100.0%)	98.9%, [89/90], (94.0%, 99.8%)	100.0%, [90/90], (95.9%, 100.0%)	98.9%, [89/90], (94.0%, 99.8%)

* For the True Negative (TN) and High Negative (HN) categories, the expected assay result was deemed to be negative. Therefore, percent agreement was calculated for negative results

Table 4: *Campylobacter* Site-to-Site Qualitative Reproducibility across sites with pooled days, runs and replicates

Category	Concentration	SITE												Total			
		2				3				5							
		Correct		Incorrect		Correct.		Incorrect		Correct		Incorrect		Correct		Incorrect	
		N	%	N	%	N	%	N	%	N	%	N	%	N	%	N	%
TN	Blank	30	100.0	0	0	30	100.0	0	0	30	100.0	0	0	90	100.0	0	0
HN	5 CFU/mL	22	73.3	8	26.7	24	80.0	6	20.0	24	80.0	6	20.0	70	77.8	20	22.2
LP	≥1 and <2 x LoD	30	100.0	0	0	30	100.0	0	0	30	100.0	0	0	90	100.0	0	0
MP	≥2 and ≤5 x LoD	30	100.0	0	0	30	100.0	0	0	30	100.0	0	0	90	100.0	0	0

Table 5: *Campylobacter* Site-to-Site Quantitative Reproducibility across sites, days, runs and within run

				Within Run Within Day		Between Run Within Day		Between Day Within Site		Between Site		Total	
Variable	Category	N	Mean	SD	%CV	SD	%CV	SD	%CV	SD	%CV	SD	%CV
Ct.Score	HN	20	36.2	0.54	1.5%	1.18	3.2%	0.00	0.0%	0.00	0.0%	1.30	3.6%
	LP	90	32.7	0.49	1.5%	0.28	0.9%	0.00	0.0%	0.00	0.0%	0.57	1.7%
	MP	90	32.2	0.60	1.8%	0.14	0.4%	0.00	0.0%	0.00	0.0%	0.61	1.9%

Table 6: *Salmonella* Site-to-Site Qualitative Reproducibility across sites with pooled days, runs, and replicates

Category	Concentration	SITE												Total			
		2				3				5							
		Correct		Incorrect		Correct.		Incorrect		Correct		Incorrect		Correct		Incorrect	
		N	%	N	%	N	%	N	%	N	%	N	%	N	%	N	%
TN	Blank	30	100.0	0	0	30	100.0	0	0	30	100.0	0	0	90	100.0	0	0
HN	75 CFU/mL	10	33.3	20	66.7	16	53.3	14	46.7	14	46.7	16	53.3	40	44.4	50	55.6
LP	≥1 and <2 x LoD	30	100.0	0	0	28	93.3	2	6.7	29	96.7	1	3.3	87	96.7	3	3.3
MP	≥2 and ≤5 x LoD	30	100.0	0	0	30	100.0	0	0	29	96.7	1	3.3	89	98.9	1	1.1

Table 7: *Salmonella* Site-to-Site Quantitative Reproducibility across sites, days, runs and within run

				Within Run Within Day		Between Run Within Day		Between Day Within Site		Between Site		Total	
Variable	Category	N	Mean	SD	%CV	SD	%CV	SD	%CV	SD	%CV	SD	%CV
Ct.Score	HN	50	36.4	0.92	2.5%	0.00	0.0%	0.00	0.0%	0.43	1.2%	1.01	2.8%
	LP	87	34.6	0.99	2.9%	0.00	0.0%	0.00	0.0%	0.61	1.8%	1.16	3.4%
	MP	89	33.2	0.61	1.9%	0.34	1.0%	0.23	0.7%	0.43	1.3%	0.85	2.6%

Table 8: *Shigella* Site-to-Site Qualitative Reproducibility across sites with pooled days, runs and replicates

Category	Concentration	SITE												Total			
		2				3				5							
		Correct		Incorrect		Correct.		Incorrect		Correct		Incorrect		Correct		Incorrect	
		N	%	N	%	N	%	N	%	N	%	N	%	N	%	N	%
TN	Blank	30	100.0	0	0	30	100.0	0	0	30	100.0	0	0	90	100.0	0	0
HN	9 CFU/mL	12	40.0	18	60.0	13	43.3	17	56.7	12	40.0	18	60.0	37	41.1	53	58.9
LP	≥1 and <2 x LoD	29	96.7	1	3.3	30	100.0	0	0	29	96.7	1	3.3	88	97.8	2	2.2
MP	≥2 and ≤5 x LoD	30	100.0	0	0	30	100.0	0	0	30	100.0	0	0	90	100.0	0	0

Table 9: *Shigella* Site-to-Site Quantitative Reproducibility across sites, days, runs and within run

				Within Run Within Day		Between Run Within Day		Between Day Within Site		Between Site		Total	
Variable	Category	N	Mean	SD	%CV	SD	%CV	SD	%CV	SD	%CV	SD	%CV
Ct.Score	HN	53	34.8	0.99	2.8%	0.57	1.6%	0.52	1.5%	0.29	0.8%	1.29	3.7%
	LP	88	33.1	0.79	2.4%	0.35	1.1%	0.23	0.7%	0.47	1.4%	1.01	3.1%
	MP	90	32.5	0.80	2.5%	0.39	1.2%	0.00	0.0%	0.50	1.5%	1.03	3.2%

Table 10: Shiga toxin Site-to-Site Qualitative Reproducibility across sites with pooled days, runs and replicates

Category	Concentration	SITE												Total			
		2				3				5							
		Correct		Incorrect		Correct.		Incorrect		Correct		Incorrect		Correct		Incorrect	
		N	%	N	%	N	%	N	%	N	%	N	%	N	%	N	%
TN	Blank	30	100.0	0	0	30	100.0	0	0	30	100.0	0	0	90	100.0	0	0
HN	100 CFU/mL	16	53.3	14	46.7	15	50.0	15	50.0	14	46.7	16	53.3	45	50.0	45	50.0
LP	≥1 and <2 x LoD	30	100.0	0	0	30	100.0	0	0	30	100.0	0	0	90	100.0	0	0
MP	≥2 and ≤5 x LoD	30	100.0	0	0	30	100.0	0	0	29	96.7	1	3.3	89	98.9	1	1.1

Table 11: Shiga toxin Site-to-Site Quantitative Reproducibility across sites, days, runs and within run

				Within Run Within Day		Between Run Within Day		Between Day Within Site		Between Site		Total	
Variable	Category	N	Mean	SD	%CV	SD	%CV	SD	%CV	SD	%CV	SD	%CV
Ct.Score	HN	45	35.9	1.78	5.0%	0.00	0.0%	0.00	0.0%	1.03	2.9%	2.06	5.7%
	LP	90	31.8	0.65	2.0%	0.00	0.0%	0.00	0.0%	0.36	1.1%	0.74	2.3%
	MP	89	31.3	0.62	2.0%	0.22	0.7%	0.07	0.2%	0.24	0.8%	0.70	2.2%

For the Lot-to-Lot reproducibility study, two users each completed a single run of 12 panel members on a single instrument for each of two lots of reagents over a 5-day period. The panels used were the same as described under the Precision heading, above. Results from 5 days of the accuracy and precision study were used to comprise data for one lot of reagents for the Lot-to-Lot study.

The overall Lot-to-Lot reproducibility percent agreement was 100% for the TN category for all targets, and ranged from 13.33% to 62.22%, 95.56% to 100% and 97.78% to 100% for the HN, LP and MP categories, respectively (**Table 12**).

Table 12: Lot-to-Lot Reproducibility Study Results using three lots of the BD MAX Enteric Bacterial Panel

Target	Level	Correct	Total	% Correct	95% CI	
					LowerCI	UpperCI
STEC	TN*	90	90	100.00%	95.91%	100.00%
	HN*	27	90	30.00%	21.51%	40.13%
	LP	89	90	98.89%	93.97%	99.80%
	MP	90	90	100.00%	95.91%	100.00%
Campy	TN	90	90	100.00%	95.91%	100.00%
	HN	56	90	62.22%	51.90%	71.54%
	LP	90	90	100.00%	95.91%	100.00%
	MP	88	90	97.78%	92.26%	99.39%
Shig	TN	90	90	100.00%	95.91%	100.00%
	HN	15	90	16.67%	10.37%	25.69%
	LP	86	90	95.56%	89.12%	98.26%
	MP	89	90	98.89%	93.97%	99.80%
Sal	TN	90	90	100.00%	95.91%	100.00%
	HN	12	90	13.33%	7.79%	21.87%
	LP	89	90	98.89%	93.97%	99.80%
	MP	90	90	100.00%	95.91%	100.00%

* For the True Negative (TN) and High Negative (HN) categories, the expected assay result was deemed to be negative. Therefore, percent agreement was calculated for negative results

Sample Storage
Specimens can be stored at 2-25 °C for a maximum of 24 hours or at 2-8 °C for a maximum of 120 hours (5 days) before testing. In case of repeat testing from the Sample Buffer Tube, the following storage conditions apply:

- within 48 hours of the steps covered in the Specimen Preparation section of the package insert, when stored at 2-25°C or
- up to 120h (5 days) after the end of the initial run when stored at 2-8°C.

Controls
External Control materials are not provided by BD; however, Quality Control strains and procedures are included in the package insert. Various types of External Controls are recommended to allow the user to select the most appropriate for their laboratory quality control program:

- Commercially available positive control materials
  - *Salmonella enterica* subsp. *enteric* serovar *Typhimurium* (ATCC 14028) containing the *SpaO* gene target.
  - *Shigella sonnei* (ATCC 9290) containing the *ipaH* gene target.
  - *E. coli*, *stx* 1a (ATCC 43890) containing the *stx* 1a gene target.
  - *Campylobacter jejuni* subsp. *jejuni* (ATCC 33291) containing the *Campylobacter* specific *tuf* gene sequence variants.

- External negative control
  - Express 10 µL of saline in the BD MAX™ Enteric Bacterial Panel SBT

The assay includes a Specimen Processing Control (SPC) that is present in the Extraction Tube. The SPC monitors DNA extraction steps, thermal cycling steps, reagent integrity and the presence of inhibitory substances.

Analytical Sensitivity
The analytical sensitivity (Limit of Detection or LoD) for the BD MAX™ Enteric Bacterial Panel was determined using two distinct target mixes of organisms. A target mix was defined as a combination of 4 target organisms that represent one strain of a genus or variant of a gene coding for a shiga-like toxin. The BD MAX™ Enteric Bacterial Panel is not designed to discriminate between the *stx*1 and *stx*2 genes. A second round of LoD testing was performed only for the *stx*1 target, without a target mix. Cultures of the target organisms were prepared and used to prepare bacterial targets that were inoculated into the SBT along with negative, pooled stool matrix (both unpreserved and Cary-Blair preserved). The negative stool matrix pool was created from stool specimens obtained from patients that were characterized by the BD MAX™ Enteric Bacterial Pane. The LoD was determined for each organism tested with both unpreserved and Cary-Blair preserved target-negative stool matrix. The results from the LoD study can be found below in **Table 13**.

Table 13: BD MAX™ Enteric Bacterial Panel Target Limits of Detection

	Unpreserved number of positive results [95% Confidence Interval]	Cary-Blair preserved number of positive results [95% Confidence Interval]
Salmonella typhimurium		
LoD (CFU/mL in SBT) [95% confidence interval]	296 [233 – 376]	193 [142 – 263]
LoD (CFU/mL in stool) [95% confidence interval]	44,400 [34,950 – 56,400]	28,950 [21,300 – 39,450]
Shigella sonnei		
LoD (CFU/mL in SBT) [95% confidence interval]	84 [59 – 118]	124 [67 – 229]
LoD (CFU/mL in stool) [95% confidence interval]	12,600 [8,850 – 17,700]	18,600 [10,050 – 34,350]
Campylobacter coli		
LoD (CFU/mL in SBT) [95% confidence interval]	95 [70 – 128]	55 [41 – 76]
LoD (CFU/mL in stool) [95% confidence interval]	14,250 [10,500 – 19,200]	8,250 [6,150 – 11,400]
E. coli stx1 / stx2		
LoD (CFU/mL in SBT) [95% confidence interval]	910 [550 – 1,505]	653 [384 – 1111]
LoD (CFU/mL in stool) [95% confidence interval]	136,500 [82,500 – 225,750]	97,950 [57,600 – 166,650]
Salmonella enteriditis		
LoD (CFU/mL in SBT) [95% confidence interval]	620 [403 – 954]	502 [345 – 729]
LoD (CFU/mL in stool) [95% confidence interval]	93,000 [60,450 – 143,100]	75,300 [51,750 – 109,350]
Shigella flexneri		
LoD (CFU/mL in SBT) [95% confidence interval]	374 [249 – 561]	229 [151 – 347]
LoD (CFU/mL in stool) [95% confidence interval]	56,100 [37,350 – 84,150]	34,350 [22,650 – 52,050]
Campylobacter jejuni		
LoD (CFU/mL in SBT) [95% confidence interval]	42 [36 – 49]	10 [9 – 10]
LoD (CFU/mL in stool) [95% confidence interval]	6,300 [5,400 – 7,350]	1,500 [1,350 – 1,500]
E. coli stx2		
LoD (CFU/mL in SBT) [95% confidence interval]	722 [519 – 1006]	599 [291 – 1231]
LoD (CFU/mL in stool) [95% confidence interval]	108,300 [77,850 – 150,900]	89,850 [43,650 – 184,650]
E. coli stx1		
LoD (CFU/mL in SBT) [95% confidence interval]	255 [195 – 332]	223 [167 – 299]
LoD (CFU/mL in stool) [95% confidence interval]	38,202 [29,259 – 49,865]	33,495 [25,026 – 44,817]

Analytical Inclusivity

The objective of this study was to demonstrate that the BD MAX™ Enteric Bacterial Panel is able to detect clinically relevant and geographically diverse serovars/strains/ subspecies for each of the BD MAX™ Enteric Bacterial Panel targets found in various geographical origins (e.g., United States, European Union, Canada, other geographical regions).

The study was designed to validate the functional performance of the BD MAX™ Enteric Bacterial Panel by verifying the specificity of the assay's primers and probes for the targeted bacterial enteric analytes [*Salmonella* spp., *Campylobacter* spp. (*jejuni* and *coli*), *Shigella* spp. and Enteroinvasive *E. coli* (EIEC)) as well as Shiga toxin-producing organisms.

One-hundred twenty-one (121) enteric target organism strains, serovars, or subspecies (**Table 14**) were included in the study at 1x the point estimate of the 95% LoD obtained in the BD MAX™ Enteric Bacterial Panel LoD study (**Table 13**). Organisms were prepared and tested as 'target mixes', consisting of one strain/serovar/ subspecies from each of the target organisms. Specimen target mixes were diluted and screened to the pre-determined, genus-specific LoD. The assay correctly identified 120 of the 121 strains tested at the LOD. One strain of *Shigella sonnei* (ENF 15987) demonstrated 79.17% positivity at a concentration of 56.1 CFU/mL. The isolate was further evaluated and yielded 100% positivity at a concentration of 405 CFU/mL. Seven (7) other strains of *Shigella sonnei* were evaluated during the analytical inclusivity study and met the study acceptance criteria at a concentration of 56.1 CFU/mL.

Table 14: Inclusivity Organisms

Organism	Organism ID
C. jejuni subsp. *doylei*	ATCC 49349
C. jejuni subsp. *doylei*	ATCC BAA-1458
C. jejuni subsp. *doylei*	BD NH[1] 450
C. jejuni subsp. *doylei*	BD NH 451
C. jejuni subsp. *doylei*	BD NH 452
C. jejuni subsp. *jejuni*	ATCC 33292
C. jejuni subsp. *jejuni*	ATCC 33560
C. jejuni subsp. *jejuni*	ATCC 35918
C. jejuni subsp. *jejuni*	ATCC 29428
C. jejuni subsp. *jejuni*	ATCC 43434
C. jejuni subsp. *jejuni*	ATCC 43435
C. jejuni subsp. *jejuni*	ATCC 43449
C. jejuni subsp. *jejuni*	ATCC 43503
C. jejuni subsp. *jejuni*	ATCC 6960
C. jejuni subsp. *jejuni*	ATCC 700819
Campylobacter coli	ATCC 43483
Campylobacter coli	ATCC 43484

Organism	Organism ID
Campylobacter coli	ATCC 43133
Campylobacter coli	ATCC 43135
Campylobacter coli	ATCC 43136
Campylobacter coli	ATCC 43472
Campylobacter coli	ATCC 43473
Campylobacter coli	ATCC 43478
Campylobacter coli	ATCC 43481
Campylobacter coli	ATCC 43482
Campylobacter coli	ATCC 43485
Campylobacter coli	ATCC 49941
Campylobacter coli	BD NH 422
Campylobacter coli	BD NH 423
Campylobacter coli	BD NH 424
Escherichia coli (EIEC)	BD ENF[2] 15626
Escherichia coli O103:H11	ATCC BAA-2215
Escherichia coli O103:H2	BD ENF15805
Escherichia coli O103:H2	ATCC BAA-2210
Escherichia coli O103:H25	ATCC BAA-2213
Escherichia coli O103:H8	BD ENF 15804
Escherichia coli O104:H21	ATCC BAA 178
Escherichia coli O111:H8	ATCC BAA-184
Escherichia coli O111:H8	ATCC BAA-2217
Escherichia coli O111:H8	ATCC BAA-179
Escherichia coli O111:NM	BD ENF15809
Escherichia coli O113:H21	ATCC BAA-177
Escherichia coli O121:H19	ATCC BAA-2219
Escherichia coli O124:NM (EIEC)	ATCC 43893
Escherichia coli O145:H25	ATCC BAA-2211
Escherichia coli O145:H28	ATCC BAA-2129
Escherichia coli O145:H48	ATCC BAA-1652
Escherichia coli O145:NM	BD ENF15811
Escherichia coli O145:NM	ATCC BAA-2222
Escherichia coli O145:NM	BD ENF15812
Escherichia coli O157	BD ENF13581
Escherichia coli O157	BD ENF 7582
Escherichia coli O157	BD ENF13568
Escherichia coli O157	BD ENF13604
Escherichia coli O157:H7	BD ENF13579

Organism	Organism ID
Escherichia coli O157:H7	ATCC 43894
Escherichia coli O157:H7	ATCC 35150
Escherichia coli O157:NM	ATCC 700376
Escherichia coli O157:NM	BD ENF10301
Escherichia coli O29:NM (EIEC)	ATCC 43892
Escherichia coli O91:H21	ATCC 51435
Escherichia coli O91:H21	ATCC 51434
Escherichia coli OX3:H21	BD ENF 15816
Salmonella agona	BD ENF 15960
Salmonella anatum	BD ENF 15961
Salmonella aareilly	ATCC 9115
Salmonella bongori	ATCC 43975
Salmonella bongori	BD ENF 16009
Salmonella araenderup	BD ENF 15962
Salmonella aholeraesuis	ATCC 7001
Salmonella enterica subsp. *arizonae*	ATCC 13314
Salmonella enterica subsp. *diarizonae*	ATCC 29226
Salmonella enterica subsp. *diarizonae*	ATCC 43973
Salmonella enterica subsp. *houtenae*	ATCC 15788
Salmonella enterica subsp. *houtenae*	ATCC 43974
Salmonella enterica subsp. *indica*	ATCC BAA-1576
Salmonella enterica subsp. *indica*	ATCC 43976
Salmonella enterica subsp. *salamae*	ATCC 43972
Salmonella hadar	ATCC 51956
Salmonella heidelberg	BD ENF15963
Salmonella infantis	ATCC 51741
Salmonella javiana	BD ENF13330
Salmonella montevideo	BD ENF 15964
Salmonella muenchen	BD ENF 8388
Salmonella newport	BD ENF15965
Salmonella oranienburg	BD ENF 7482
Salmonella paratyphi A	ATCC 9150
Salmonella paratyphi B	ATCC 51962
Salmonella saintpaul	BD ENF 15967
Salmonella schwarzengrund	BD ENF 7452
Salmonella thompson	BD ENF 15968
Salmonella typhi	ATCC 10749
Salmonella virchow	ATCC 51955

Organism	Organism ID
Shigella boydii	ATCC 12028
Shigella boydii	ATCC 8700
Shigella boydii	ATCC 9207
Shigella boydii	BD ENF 15975
Shigella boydii	BD ENF 15976
Shigella dysenteriae	ATCC 11835
Shigella dysenteriae	ATCC 13313
Shigella dysenteriae	ATCC 9361
Shigella dysenteriae	BD ENF 2932
Shigella dysenteriae	BD ENF 15977
Shigella flexneri	ATCC 29903
Shigella flexneri	ATCC 33948
Shigella flexneri	BD ENF 2900
Shigella flexneri	BD ENF 7419
Shigella flexneri	ATCC 12022
Shigella flexneri	BD ENF 15983
Shigella flexneri	BD ENF 15984
Shigella flexneri	BD ENF 15985
Shigella flexneri	BD ENF 15428
Shigella flexneri	BD ENF 2903
Shigella sonnei	ATCC 13096
Shigella sonnei	ATCC 25931
Shigella sonnei	BD ENF 5704
Shigella sonnei	BD ENF 8063
Shigella sonnei	BD ENF 15986
Shigella sonnei	BD ENF 15987
Shigella sonnei	BD ENF 15988
Shigella sonnei	ATCC 29930

[1]BD NH – BD internal strain designation

[2]BD ENF – BD internal strain designation

Analytical Specificity

The BD MAX™ Enteric Bacterial Panel was performed on samples containing phylogenetically related species and other organisms (bacteria, viruses, parasites and yeast) likely to be found in stool specimens.

- Nine (9) out of 9 *Campylobacter* strains (*Campylobacter* species other than *C. jejuni* or *C. coli*) with undetectable *tuf* gene sequences, tested at a concentration ≥ 1 x 10^5 CFU/mL per SBT, produced negative results with the BD MAX™ Enteric Bacterial Panel.
- Six (6) out of 6 *E. coli* strains other than Shiga toxin-producing strains, tested at a concentration ≥ 1 x 10^5 CFU/mL of SBT, produced negative results with the BD MAX™ Enteric Bacterial Panel.
- Ninety-eight (98) out of 99 other bacterial strains (including 53 species and subspecies), tested at a concentration ≥ 1 x 10^6 CFU/mL of SBT (or ~ 1 x 10^8 genomic DNA cp/mL or 1 x 10^8 elementary bodies/mL of SBT), produced negative results with the BD MAX™ Enteric Bacterial Panel. *S. boydii* (ATCC 12028) produced 1 replicate out of 3 as positive for the presence of *stx*.
- Fifteen (15) out of 15 viruses, tested at a concentration ≥ 1 x 10^4 PFU/mL of SBT, produced negative results with the BD MAX™ Enteric Bacterial Panel.
- Three (3) out of 3 ova and parasites, tested at a concentration ≥ 1 x 10^5 cysts/mL of SBT, produced negative results with the BD MAX™ Enteric Bacterial Panel.
- Sixteen (16) Enteric organisms representing each target of the BD MAX™ Enteric Bacterial Panel were tested, with results as follows:
    - Three (3) of 3 *Campylobacter* spp.; one *C. coli*, one *C. jejuni*, subsp. *doylei* and one *C. jejuni*, subsp. *jejuni* bearing the *tuf* gene tested at a concentration ≥ 1 x 10^6 CFU/mL of SBT, produced positive results for *Campylobacter* and negative results for all other targets with the BD MAX™ Enteric Bacterial Panel.
    - Four (4) of 4 *E. coli*; two O157 and two non-O157 strains bearing the *stx* gene tested at a concentration ≥ 1 x 10^6 CFU/mL of SBT, produced positive results for *E. coli* and negative results for all other targets with the BD MAX™ Enteric Bacterial Panel.
    - Five (5) of 5 *Salmonella* spp. bearing the *spaO* gene tested at a concentration≥ 1 x 10^6 CFU/mL of SBT, produced positive results for *Salmonella* and negative results for all other targets with the BD MAX™ Enteric Bacterial Panel.
    - Three (3) of 4 *Shigella* spp.; one *S. sonnei*, one *S. boydii*, one *S. flexneri* and *S. dysentariae* bearing the *ipaH* gene tested at a concentration ≥ 1 x 10^6 CFU/mL of SBT, produced positive results for *ipaH* and negative results for all other targets with the BD MAX™ Enteric Bacterial Panel.
        - Initial testing of *S. boydii* (ATCC 12028) produced 1 replicate out of 3 as positive for the presence of *stx*. Subsequent testing of this strain produced positive results with 8 out of 20 replicates for the presence of *stx*.

Interfering Substances

Nineteen (19) biological and chemical substances occasionally used or found in stool specimens were evaluated for potential interference with the BD MAX Enteric Bacterial Panel. Included in this study was an Antibiotics Mixture, which consisted of a combination of 8 different antibiotics, tested simultaneously, with each antibiotic at a concentration that may be excreted in a stool sample. Vagisil was identified as a potentially interfering substance at a concentration of 9.2% Vagisil in a stool sample or 0.92 mg/mL of SBT. Nystatin cream and spermicidal lubricant both demonstrated potential interference at a concentration of 50% (5.0 mg/mL of interferent in the SBT). The BD MAX Enteric Bacterial Panel demonstrated acceptable performance with nystatin cream at a concentration of 31% (3.1 mg/mL of nystatin cream in the SBT) and spermicidal lubricant at 34% (3.4 mg/mL of spermicidal lubricant in the SBT). Results demonstrated no reportable interference with any other substance tested (**Table 15**).

Table 15: Endogenous and Commercial Exogenous Substances tested with the BD MAX Enteric Bacterial Panel

Brand Name or Description	Result	Brand Name or Description	Result
Fecal Fat	NI	Spermicidal Lubricant	P
Human DNA	NI	Diaper Rash Cream	NI
Mucus	NI	Vagisil	I
Whole human blood	NI	Laxatives	NI
Hydrocortisone Cream	NI	Anti-Diarrheal (liquid)	NI
Antiseptic Towelettes	NI	Anti-Diarrheal (pill)	NI
Enema	NI	Antibiotics Mixture	NI
Hemorrhoidal Gel	NI	Antacids	NI
Nystatin Cream	P	Non-Steroidal Anti-Inflammatory (NSAID)	NI
Topical Antibiotic	NI		

I: Interference with the BD MAX Enteric Bacterial Panel.
P: Potential interference with the BD MAX Enteric Bacterial Panel at high concentrations
NI: No reportable interference with the BD MAX Enteric Bacterial Panel.

Carryover / Cross-Contamination

A study was conducted to investigate the potential for cross-contamination between high positive and negative specimens throughout the BD MAX™ Enteric Bacterial Panel workflow. Of one-hundred sixty-seven (167) valid results, one-hundred sixty-six (166) valid negative results were reported for all targets. Four (4) false positive results were reported overall, all from 1 sample tube. The overall contamination rate was 0.6% for all targets, and for the study as a whole.

Mixed Infection/Competitive Interference

The mixed infection/competitive interference study was designed to evaluate the ability of the BD MAX Enteric Bacterial Panel to detect low positive results in the presence of other targets at high concentrations. Four (4) organisms (*Salmonella typhimurium*, *Campylobacter coli*, *Shigella sonnei* and *E. coli* O157:H7) were individually prepared at 1.5X their respective LoD to serve as a low target in the BD MAX Enteric Bacterial Panel SBT. A high target mix comprised of the organisms representative of the other three BD MAX Enteric Bacterial Panel analytes at a concentration of > $1x10^6$ CFU/mL in the SBT was spiked into the SBT along with 10 µL of unpreserved stool and tested to simulate mixed infections. All four low target organisms were successfully detected by the BD MAX Enteric Bacterial Panel when combined with their respective simulated high target concentration mixed infection preparations.

Clinical Performance Studies

The Clinical Accuracy study was designed to assess the performance of the BD MAX™ Enteric Bacterial Panel for the identification of *Campylobacter* (*jejuni* & *coli*), *Salmonella* spp., *Shigella* spp. and EIEC as well as shiga toxin-producing organisms , from unpreserved or Cary-Blair preserved soft to diarrheal stool specimens. This multicenter study evaluated results obtained with the BD MAX Enteric Bacterial Panel compared to those obtained with the reference method. Clinical centers were employed to collect and test patient specimens; whereas collection centers were employed to collect and test patient specimens using the reference method, with BD MAX™ Enteric Bacterial Panel testing being performed by a testing center.

The study involved a total of eight (8) geographically diverse clinical centers where specimens were collected as part of routine patient care, enrolled into the trial, and tested on the BD MAX™ Enteric Bacterial Panel. Only excess, de-identified patient specimens were used. Additionally, an internal site was involved as a clinical center to perform BD MAX™ testing on specimens supplied by other collection centers.

Clinical centers were selected for the clinical study based on a number of criteria, such as investigator and site personnel availability, number of specimens of interest tested for each target, prevalence, and familiarity with PCR methodology. The clinical centers were also selected according to the specimen types that they routinely collect. Collection centers were selected for their high level of similarity with clinical centers in the culture and identification methods used for the study targets. Clinical centers utilizing methodologies that did not have a high degree of similarity sent specimens to a central laboratory for reference method testing. Prospective (fresh) specimens collected at the collection centers consisted of a mix of Cary-Blair preserved and unpreserved specimens, and were not pre-selected but rather collected on an "all-comers" basis between June and September, 2013. Accordingly, the specimens were enrolled as prospective specimens.

Retrospective (frozen) specimens were collected from sites between March 2012 and August 2013. Further, one site enrolled unpreserved specimens collected and archived from June to September 2007 and from October to December 2011. Inclusion and exclusion criteria were identical to those as for prospective specimens. Retrospective specimens were stored frozen (-20 °C or lower) after collection and did not undergo

freeze-thaw cycles. Specimens were thawed at the time of testing with the BD MAX™ Enteric Bacterial Panel.

For retrospective specimens, the historical culture results were recorded at the collection site and the specimens were not re-cultured. The historical culture results were confirmed using an alternate PCR and bi-directional amplicon sequencing as part of the composite reference method in order to confirm the presence of target DNA.

A total of 3457 prospective specimens (2112 Cary-Blair preserved and 1345 unpreserved) and 785 retrospective specimens (464 Cary-Blair preserved and 321 unpreserved) were enrolled. **Table 16** below presents the number of prospective compliant specimens for which a reportable (positive or negative) result was obtained by the reference method and for which a reportable result was obtained by the BD MAX EBP (i.e., the total compliant dataset used for PPA and NPA calculations), by target and specimen type. A total of 104 retrospective specimens were not included in the performance calculations below as the historical results were not confirmed by an alternate PCR and bi-directional sequencing.

Table 16: Summary of Prospective Enrollment, by Target and Specimen Type

	Campylobacter	*Shigella*	*Salmonella*	Shigatoxins
Positive				
Cary-Blair	26	19	20	8
Unpreserved	22	22	24	2
Sub-Total	48	41	44	10
Negative				
Cary-Blair	1774	1809	1808	1781
Unpreserved	1216	1219	1215	711
Sub-Total	2990	3028	3023	2492
Grand Total	3038	3069	3067	2502

Table 17 describes the number of compliant specimens enrolled by patient age and specimen type. A total of 104 retrospective specimens were not included in the performance calculations below as the historical results were not confirmed by an alternate PCR and bi-directional sequencing. **Tables 19** through **22** describe the performance characteristics of the BD MAX™ Enteric Bacterial Panel that were observed during the clinical trial.

Table 17: Compliant clinical trial enrollment summary by age group and specimen type

Age Group	Cary-Blair Preserved	Unpreserved	Combined
< 1	110	43	153
1-4	302	128	430
5-12	270	209	479
13-18	271	168	439
19-65	1222	799	2021
Over 65	388	249	637
Unknown	3	2	5
Total	2566	1598	4164

Table 18 below presents the number of compliant specimens for which historical routine results were confirmed by the confirmatory method (i.e. alternate PCR and bi-directional amplicon sequencing) and for which a reportable result was obtained by the BD MAX EBP (i.e., the total compliant dataset used for PPA and NPA calculations), by target and specimen type.

Table 18: Summary of Retrospective (Frozen) Enrollmen

	Campylobacter	*Shigella*	*Salmonella*	Shigatoxins
Positive				
Cary-Blair	66	51	106	41
Unpreserved	67	41	61	25
Sub-Total	133	92	167	66
Negative				
Cary-Blair	151	187	213	79
Unpreserved	223	264	238	11
Sub-Total	374	451	451	90
Grand Total	507	543	618	156

For the Cary-Blair preserved specimen type, the BD MAX Enteric Bacterial Panel identified 96.2% and 98.7% of the *Campylobacter* spp. prospective positive and negative specimens, respectively, and 97% and 100% of the retrospective positive and negative specimens, respectively. For the unpreserved specimen type, the BD MAX Enteric Bacterial Panel identified 100% and 97.5% of the *Campylobacter* spp. prospective positive and negative specimens, respectively, and 97% and 99.1% of the retrospective positive and negative specimens, respectively (**Table 19**).

Table 19: *Campylobacter* spp. - Overall Performance

Specimen Type	Specimen Origin	BD MAX	RM		Total
			P	N	
Cary-Blair	Prospective (Fresh)	P	25	23[2]	*48*
		N	1[1]	1751	*1752*
		Total	*26*	*1774*	*1800*
PPA (95% CI): 96.2% (81.1%, 99.3%) NPA (95% CI): 98.7% (98.1%, 99.1%)					
Cary-Blair	Retrospective (Frozen)	P	64	0	*64*
		N	2	151	*153*
		Total	*66*	*151*	*217*
PPA (95% CI): 97% (89.6%, 99.2%) NPA (95% CI): 100% (97.5%, 100%)					
Unpreserved	Prospective (Fresh)	P	22	31[3]	*53*
		N	0	1185	*1185*
		Total	*22*	*1216*	*1238*
PPA (95% CI): 100% (85.1%, 100%) NPA (95% CI): 97.5% (96.4%, 98.2%)					
Unpreserved	Retrospective (Frozen)	P	65	2	*67*
		N	2	221	*223*
		Total	*67*	*223*	*290*
PPA (95% CI): 97% (89.8%, 99.2%) NPA (95% CI): 99.1% (96.8%, 99.8%)					

[1] This specimen was also tested using an alternate PCR assay followed by bi-directional sequencing and gave a negative result.
[2] These twenty-three (23) specimens were also tested using an alternate PCR assay followed by bi-directional sequencing; ten (10) of twenty-three (23) gave a positive result.
[3] These thirty-one (31) specimens were also tested using an alternate PCR assay followed by bi-directional sequencing; fourteen (14) of thirty-one (31) gave a positive result.

For the Cary-Blair preserved specimen type, the BD MAX Enteric Bacterial Panel identified 85% and 99.1% of the *Salmonella* spp. prospective positive and negative specimens, respectively, and 99.1% and 100% of the retrospective positive and negative specimens, respectively. For the unpreserved specimen type, the BD MAX Enteric Bacterial Panel identified 91.7% and 98.9% of the *Salmonella* spp. prospective positive and negative specimens, respectively, and 100% and 99.6% of the retrospective positive and negative specimens, respectively (**Table 20**).

Table 20: *Salmonella* spp. – Overall Performance

Specimen Type	Specimen Origin	BD MAX	RM		Total
			P	N	
Cary-Blair	Prospective (Fresh)	P	17	17[2]	*34*
		N	3[1]	1791	*1794*
		Total	*20*	*1808*	*1828*
PPA (95% CI): 85% (64%, 94.8%) NPA (95% CI): 99.1% (98.5%, 99.4%)					
Cary-Blair	Retrospective (Frozen)	P	105	0	105
		N	1	213	214
		Total	*106*	213	319
PPA (95% CI): 99.1% (94.8%, 99.8%) NPA (95% CI): 100% (98.2%, 100%)					
Unpreserved	Prospective (Fresh)	P	22	13[3]	*35*
		N	2[1]	1202	*1204*
		Total	*24*	*1215*	*1239*
PPA (95% CI): 91.7% (74.2%, 97.7%) NPA (95% CI): 98.9% (98.2%, 99.4%)					
Unpreserved	Retrospective (Frozen)	P	61	1	*62*
		N	0	237	*237*
		Total	*61*	*238*	*299*
PPA (95% CI): 100% (94.1%, 100%) NPA (95% CI): 99.6% (97.7%, 99.9%)					

[1] These three (3) specimens were also tested using an alternate PCR assay followed by bi-directional sequencing and gave a negative result.
[2] These seventeen (17) specimens were also tested using an alternate PCR assay followed by bi-directional sequencing; eleven (11) of seventeen (17) gave a positive result.
[3] These thirteen (13) specimens were also tested using an alternate PCR assay followed by bi-directional sequencing; eleven (11) of thirteen (13) gave a positive result.

For the Cary-Blair preserved specimen type, the BD MAX Enteric Bacterial Panel identified 100% and 99.7% of the *Shigella* spp. / EIEC organisms prospective positive and negative specimens, respectively, and 98% and 100% of the retrospective positive and negative specimens, respectively. For the unpreserved specimen type, the BD MAX Enteric Bacterial Panel identified 100% and 99.4% of the *Shigella* spp. / EIEC organisms prospective positive and negative specimens, respectively, and 100% and 100% of the retrospective positive and negative specimens, respectively (**Table 21**).

Table 21: *Shigella* spp. / EIEC – Overall Performance

Specimen Type	Specimen Origin	BD MAX	RM		Total
			P	N	
Cary-Blair	Prospective (Fresh)	P	19	5[1]	*24*
		N	0	1804	*1804*
		Total	*19*	*1809*	*1828*
PPA (95% CI): 100% (83.2%, 100%) NPA (95% CI): 99.7% (99.4%, 99.9%)					
Cary-Blair	Retrospective (Frozen)	P	50	0	*50*
		N	1	187	*188*
		Total	*51*	*187*	*238*
PPA (95% CI): 98% (89.7%, 99.7%) NPA (95% CI): 100% (98%, 100%)					
Unpreserved	Prospective (Fresh)	P	22	7[2]	*29*
		N	0	1212	*1212*
		Total	*22*	*1219*	*1241*
PPA (95% CI): 100% (85.1%, 100%) NPA (95% CI): 99.4% (98.8%, 99.7%)					
Unpreserved	Retrospective (Frozen)	P	41	0	*41*
		N	0	264	*264*
		Total	*41*	*264*	*305*
PPA (95% CI): 100% (91.4%, 100%) NPA (95% CI): 100% (98.6%, 100%)					

[1] These five (5) specimens were also tested using an alternate PCR assay followed by bi-directional sequencing; all five (5) specimens gave a positive result.
[2] These seven (7) specimens were also tested using an alternate PCR assay followed by bi-directional sequencing; six (6) of seven (7) gave a positive result.

For the Cary-Blair preserved specimen type, the BD MAX Enteric Bacterial Panel identified 75% and 99.3% of the Shiga toxins (*stx*1/*stx*2) prospective positive and negative specimens, respectively, and 100% and 100% of the retrospective positive and negative specimens, respectively. For the unpreserved specimen type, the BD MAX Enteric Bacterial Panel identified 100% and 99% of the Shiga toxins (*stx*1 and/or *stx*2) prospective positive and negative specimens, respectively, and 100% and 100% of the retrospective positive and negative specimens, respectively (**Table 22**).

Table 22: Shiga toxins (*stx1/stx2*) – Overall Performance

Specimen Type	Specimen Origin	BD MAX	RM		Total
			P	N	
Cary-Blair	Prospective (Fresh)	P	6	13[2]	*19*
		N	2[1]	1768	*1770*
		Total	*8*	*1781*	*1789*
PPA (95% CI): 75% (40.9%, 92.9%) NPA (95% CI): 99.3% (98.8%, 99.6%)					
Cary-Blair	Retrospective (Frozen)	P	41	0	*41*
		N	0	*79*	*79*
		Total	*41*	*79*	*120*
PPA (95% CI): 100% (91.4%, 100%) NPA (95% CI): 100% (95.4%, 100%)					
Unpreserved	Prospective (Fresh)	P	2	7[3]	*9*
		N	0	704	*704*
		Total	*2*	*711*	*713*
PPA (95% CI): 100% (34.2%, 100%) NPA (95% CI): 99% (98%, 99.5%)					
Unpreserved	Retrospective (Frozen)	P	25	0	*25*
		N	0	11	*11*
		Total	*25*	*11*	*36*
PPA (95% CI): 100% (86.7%, 100%) NPA (95% CI): 100% (74.1%, 100%)					

[1] These two (2) specimens were also tested using an alternate PCR assay followed by bi-directional sequencing and gave a negative result.
[2] These thirteen (13) specimens were also tested using an alternate PCR assay followed by bi-directional sequencing; seven (7) of thirteen (13) gave a positive result.
[3] These seven (7) specimens were also tested using an alternate PCR assay followed by bi-directional sequencing; three (3) of seven (7) gave a positive result.

Performance of the BD MAX Enteric Bacterial Panel by species/toxin type as observed during the clinical trial is presented below in **Tables 23** through **25**. The species identification was obtained either from the culture and identification portion of the reference method testing or from sequencing performed for the confirmation of retrospective specimen historical results and on discrepant prospective specimens. While the BD MAX Enteric Bacterial Panel is designed to detect the species and toxin types described below, the panel does not report results to the species or toxin level.

Table 23: *Campylobacter* performance per species observed during the clinical trial

Campylobacter			PPA	
Specimen Type	**Specimen Origin**	**Species**	**Estimate**	**95% CI**
Cary-Blair Preserved	Prospective (Fresh)	*jejuni*[1]	95.8% (23/24)	(79.8%, 99.3%)
		Untyped	100.0% (2/2)	(34.2%, 100.0%)
	Retrospective (Frozen) Prospective (Fresh)	*coli*	100.0% (2/2)	(34.2%, 100.0%)
		jejuni	96.9% (62/64)	(89.3%, 99.1%)
Unpreserved	Prospective Retrospective (Frozen)	*jejuni*	100.0% (19/19)	(83.2%, 100.0%)
		jejuni or *coli*	100.0% (1/1)	(20.7%, 100.0%)
		Untyped	100.0% (2/2)	(34.2%, 100.0%)
	Prospective (Fresh)	*coli*	100.0% (5/5)	(56.6%, 100.0%)
		jejuni	96.8% (60/62)	(89.0%, 99.1%)

[1] Of these specimens, one (1) prospective specimen was also tested using a validated PCR assay followed by bi-directional sequencing and gave a negative result.

Table 24: *Shigella* performance per species type observed during the clinical trial

Shigella			PPA	
Specimen Type	**Specimen Origin**	**Species**	**Estimate**	**95% CI**
Cary-Blair Preserved	Prospective (Fresh)	*flexneri*	100.0% (1/1)	(20.7%, 100.0%)
		sonnei	100.0% (18/18)	(82.4%, 100.0%)
	Retrospective (Frozen)	*sonnei*	98.0% (50/51)	(89.7%, 99.7%)
Unpreserved	Prospective (Fresh)	*flexneri*	100.0% (2/2)	(34.2%, 100.0%)
		sonnei	100.0% (20/20)	(83.9%, 100.0%)
	Retrospective (Frozen)	*flexneri*	100.0% (1/1)	(20.7%, 100.0%)
		sonnei	100.0% (40/40)	(91.2%, 100.0%)

Table 25: Shiga toxins performance per toxin type observed during the clinical trial

Shiga toxins			PPA	
Specimen Type	**Specimen Origin**	**Toxin Type**	**Estimate**	**95% CI**
Cary-Blair Preserved	Prospective (Fresh)	*stx*1	100.0% (4/4)	(51.0%, 100.0%)
		*stx*2	100.0% (1/1)	(20.7%, 100.0%)
		*stx*1 and *stx*2[1]	33.3% (1/3)	(6.1%, 79.2%)
	Retrospective (Frozen)	*stx*1	100.0% (28/28)	(87.9%, 100.0%)
		*stx*2	100.0% (6/6)	(61.0%, 100.0%)
		*stx*1 and *stx*2	100.0% (7/7)	(64.6%, 100.0%)
Unpreserved	Prospective (Fresh)	*stx*1	100.0% (1/1)	(20.7%, 100.0%)
		*stx*1 and *stx*2	100.0% (1/1)	(20.7%, 100.0%)
	Retrospective (Frozen)	*stx*1	100.0% (5/5)	(56.6%, 100.0%)
		*stx*2	100.0% (6/6)	(61.0%, 100.0%)
		*stx*1 and *stx*2	100.0% (14/14)	(78.5%, 100.0%)

[1] Two (2) prospective specimens were also tested using a validated PCR assay followed by bi-directional sequencing and gave a negative result.

Table 26 below shows the co-infections detected by the BD MAX Enteric Bacterial Panel during the prospective segment of the clinical trial. Note that there were no co-infections detected by the reference method during the prospective segment of the clinical trial.

Table 26: Co-infections observed during the BD MAX Enteric Bacterial Panel prospective clinical trial

Distinct Co-infection Combinations Detected by BD MAX Enteric Bacterial Assay		Number of Discrepant Co-Infections	Discrepant Analyte(s)[1]
Analyte 1	**Analyte 2**		
Shigella	*stx*	1	*stx*[2]
stx	*Campylobacter*	1	*stx*[3]
stx	*Salmonella*	2	*stx* (2) and *Salmonella* (1)[4]
Campylobacter	*Salmonella*	2	*Campylobacter* (2), *Salmonella* (1)[5]

[1] A discrepant co-infection or discrepant analyte was defined as one that was detected by the BD MAX assay but not detected by the reference method.
[2] One (1) discrepant *stx* was investigated using an alternate method; bi-directional sequence analysis identified the analyte in 0/1 cases.
[3] One (1) discrepant *stx* was investigated using an alternate method; bi-directional sequence analysis identified the analyte in 1/1 cases.
[4] Two (2) discrepant *stx* were investigated using an alternate method; bi-directional sequence analysis identified the analyte in 0/2 cases. One (1) discrepant *Salmonella* was investigated using an alternate method; bi-directional sequence analysis identified the analyte in 1/1 cases.
[5] Two (2) discrepant *Campylobacter* were investigated using an alternate method; bi-directional sequence analysis identified the analyte in 0/2 cases. One (1) discrepant *Salmonella* was investigated using an alternate method; bi-directional sequence analysis identified the analyte in 0/1 cases.

Of the 3183 prospective specimens initially evaluated with the BD MAX™ Enteric Bacterial Panel, 4.0% of the Cary-Blair preserved and 7.8% of the unpreserved specimens initially reported as Unresolved. Following a valid repeat test, 0.1% of the Cary-Blair preserved and 1.0% of the unpreserved specimens remained Unresolved. Of the 783 retrospective specimens initially evaluated with the BD MAX™ Enteric Bacterial Panel, 2.2% of the Cary-Blair preserved and 4.1% of the unpreserved specimens initially reported as Unresolved. Following a valid repeat test, 0.2% of the Cary-Blair preserved and 0.6% of the unpreserved specimens remained Unresolved (**Table 27**). The total numbers provided in **Table 27** are based on compliant specimens and BD MAX™ Enteric Bacterial Panel results.

Table 27: Unresolved Rates

		Initial Unresolved Rates		**Unresolved Rates After Repeat**	
Specimen Type	**Specimen Origin**	**Percent**	**95% CI**	**Percent**	**95% CI**
Cary-Blair	Prospective (Fresh)	4.0% (77/1905)	(3.2%, 5.0%)	0.1% (2/1897)	(0.0%, 0.4%)
	Retrospective (Frozen)	2.2% (10/464)	(1.2%, 3.9%)	0.2% (1/463)	(0.0%, 1.2%)
Unpreserved	Prospective (Fresh)	7.8% (100/1278)	(6.5%, 9.4%)	1.0% (13/1251)	(0.6%, 1.8%)
	Retrospective (Frozen)	4.1% (13/319)	(2.4%, 6.8%)	0.6% (2/317)	(0.2%, 2.3%)

Of the 3183 prospective specimens initially evaluated with the BD MAX™ Enteric Bacterial Panel, 1.7% of the Cary-Blair preserved and 1.6% of the unpreserved specimens initially reported as Indeterminate. Following a valid repeat test, 0% of the Cary-Blair preserved and 0.2% of the unpreserved specimens remained Indeterminate. Of the 783 retrospective specimens initially evaluated with the BD MAX™ Enteric Bacterial Panel, 1.5% of the Cary-Blair preserved and 1.9% of the unpreserved specimens initially reported as Indeterminate. Following a valid repeat test, 0% of the Cary-Blair preserved and 0% of the unpreserved specimens remained Indeterminate (**Table 28**). The total numbers provided in **Table 28** are based on compliant specimens and BD MAX™ Enteric Bacterial Panel results.

Table 28: Indeterminate Rates

		Initial Indeterminate Rates		**Final Indeterminate Rates After Repeat**	
Specimen Type	**Specimen Origin**	**Percent**	**95% CI**	**Percent**	**95% CI**
Cary-Blair	Prospective (Fresh)	1.7% (33/1905)	(1.2%, 2.4%)	0.0% (0/1897)	(0.0%, 0.2%)
	Retrospective (Frozen)	1.5% (7/464)	(0.7%, 3.1%)	0.0% (0/463)	(0.0%, 0.8%)
Unpreserved	Prospective (Fresh)	1.6% (20/1278)	(1.0%, 2.4%)	0.2% (2/1251)	(0.0%, 0.6%)
	Retrospective (Frozen)	1.9% (6/319)	(0.9%, 4.0%)	0.0% (0/317)	(0.0%, 1.2%)

Of the 3183 prospective specimens initially evaluated with the BD MAX™ Enteric Bacterial Panel, 1.3% of the Cary-Blair preserved and 2.0% of the unpreserved specimens initially reported as Incomplete. Following a valid repeat test, 0% of the Cary-Blair preserved and 0% of the unpreserved specimens remained Incomplete. Of the 783 retrospective specimens initially evaluated with the BD MAX™ Enteric Bacterial Panel, 1.3% of the Cary-Blair preserved and 0% of the unpreserved specimens initially reported as Unresolved. Following a valid repeat test, 0% of the Cary-Blair preserved specimens remained Incomplete (**Table 29**). The total numbers provided in **Table 29** are based on compliant specimens and BD MAX™ Enteric Bacterial Panel results.

Table 29: Incomplete Rates

		Initial Incomplete Rates		Final Incomplete Rates After Repeat	
Specimen Type	Specimen Origin	Percent	95% CI	Percent	95% CI
Cary-Blair	Prospective (Fresh)	1.3% (24/1905)	(0.8%, 1.9%)	0.0% (0/1897)	(0.0%, 0.2%)
	Retrospective (Frozen)	1.3% (6/464)	(0.6%, 2.8%)	0.0% (0/463)	(0.0%, 0.8%)
Unpreserved	Prospective (Fresh)	2.0% (26/1278)	(1.4%, 3.0%)	0.0% (0/1251)	(0.0%, 0.3%)
	Retrospective (Frozen)	0.0% (0/319)	(0.0%, 1.2%)	0.0% (0/317)	(0.0%, 1.2%)

Expected Values

In the BD MAX Enteric Bacterial Panel clinical study, reportable results from compliant specimens, were obtained from 8 geographically diverse sites and compared to the reference methods. The study population was grouped based on specimen type. The number and percentage of positive cases by target, as determined by the BD MAX Enteric Bacterial Panel during the prospective segment of the clinical trial, are presented below in **Table 30**.

Table 30: Observed Prevalence by Target and Specimen Type

		Prevalence			
Specimen Type	**Site**	***Salmonella***	***Shigella*/EIEC**	***Campylobacter***	**Shiga toxins**
Cary-Blair Preserved	1	0.0% (0/186)	0.0% (0/186)	1.1% (2/188)	0.0% (0/185)
	2	0.8% (3/377)	0.3% (1/377)	1.6% (6/368)	0.8% (3/391)
	3	0.9% (5/548)	0.2% (1/548)	0.8% (4/528)	0.2% (1/551)
	4	3.9% (6/152)	11.2% (17/152)	2.0% (3/152)	0.0% (0/135)
	5	0.3% (1/339)	0.0% (0/339)	1.5% (5/340)	0.3% (1/320)
	6	1.4% (6/431)	0.0% (0/431)	1.9% (8/431)	0.7% (3/411)
	Total	1.0% (21/2033)	0.9% (19/2033)	1.4% (28/2007)	0.4% (8/1993)
Unpreserved	1	1.6% (6/376)	0.3% (1/376)	0.8% (3/376)	0.0% (0/176)
	7	1.6% (5/305)	0.0% (0/305)	2.0% (6/304)	0.0% (0/229)
	8	1.4% (4/284)	0.0% (0/284)	1.1% (3/284)	0.4% (1/265)
	4	2.9% (9/314)	6.7% (21/314)	3.5% (11/314)	0.4% (1/266)
	Total	1.9% (24/1279)	1.7% (22/1279)	1.8% (23/1278)	0.2% (2/936)

DEPARTMENT OF HEALTH & HUMAN SERVICES

Public Health Service

Food and Drug Administration
10903 New Hampshire Avenue
Document Control Center – WO66-G609
Silver Spring, MD 20993-0002

BECTON, DICKINSON AND COMPANY
PAUL SWIFT
REGULATORY AFFAIRS PROJECT MANAGER
7 LOVETON CIRCLE
SPARKS MD 21152

May 06, 2014

Re: K140111
Trade/Device Name: BD MAX™ Enteric Bacterial Panel
Regulation Number: 21 CFR 866.3990
Regulation Name: Gastrointestinal microorganism multiplex nucleic acid-based assay
Regulatory Class: II
Product Code: PCI, PCH, OOI
Dated: April 25, 2014
Received: April 28, 2014

Dear Mr. Swift:

We have reviewed your Section 510(k) premarket notification of intent to market the device referenced above and have determined the device is substantially equivalent (for the indications for use stated in the enclosure) to legally marketed predicate devices marketed in interstate commerce prior to May 28, 1976, the enactment date of the Medical Device Amendments, or to devices that have been reclassified in accordance with the provisions of the Federal Food, Drug, and Cosmetic Act (Act) that do not require approval of a premarket approval application (PMA). You may, therefore, market the device, subject to the general controls provisions of the Act. The general controls provisions of the Act include requirements for annual registration, listing of devices, good manufacturing practice, labeling, and prohibitions against misbranding and adulteration. Please note: CDRH does not evaluate information related to contract liability warranties. We remind you, however, that device labeling must be truthful and not misleading.

If your device is classified (see above) into either class II (Special Controls) or class III (PMA), it may be subject to additional controls. Existing major regulations affecting your device can be found in the Code of Federal Regulations, Title 21, Parts 800 to 898. In addition, FDA may publish further announcements concerning your device in the Federal Register.

Please be advised that FDA's issuance of a substantial equivalence determination does not mean that FDA has made a determination that your device complies with other requirements of the Act or any Federal statutes and regulations administered by other Federal agencies. You must comply with all the Act's requirements, including, but not limited to: registration and listing (21 CFR Part 807); labeling (21 CFR Parts 801 and 809); medical device reporting (reporting of medical device-related adverse events) (21 CFR 803); good manufacturing practice requirements as set forth in the quality systems (QS) regulation (21 CFR Part 820); and if applicable, the electronic product radiation control provisions (Sections 531-542 of the Act); 21 CFR 1000-1050.

If you desire specific advice for your device on our labeling regulations (21 CFR Parts 801 and 809), please contact the Division of Industry and Consumer Education at its toll-free number (800) 638 2041 or (301) 796-7100 or at its Internet address http://www.fda.gov/MedicalDevices/ResourcesforYou/Industry/default.htm. Also, please note the regulation entitled, "Misbranding by reference to premarket notification" (21CFR Part 807.97). For questions regarding the reporting of adverse events under the MDR regulation (21 CFR Part 803), please go to http://www.fda.gov/MedicalDevices/Safety/ReportaProblem/default.htm for the CDRH's Office of Surveillance and Biometrics/Division of Postmarket Surveillance.

You may obtain other general information on your responsibilities under the Act from the Division of Industry and Consumer Education at its toll-free number (800) 638-2041 or (301) 796-7100 or at its Internet address http://www.fda.gov/MedicalDevices/ResourcesforYou/Industry/default.htm.

Sincerely yours,

John Hobson -S for

Sally Hojvat, M.Sc., PhD
Director
Division of Microbiology Devices
Office of In Vitro Diagnostics
and Radiological Health
Center for Devices and Radiological Health

Enclosure

DEPARTMENT OF HEALTH AND HUMAN SERVICES
Food and Drug Administration

Indications for Use

Form Approved: OMB No. 0910-0120
Expiration Date: January 31, 2017
See PRA Statement on last page.

510(k) Number *(if known)*

K140111

Device Name

BD MAX™ Enteric Bacterial Panel

Indications for Use *(Describe)*

The BD MAX™ Enteric Bacterial Panel performed on the BD MAX™ System is an automated *in vitro* diagnostic test for the direct qualitative detection and differentiation of enteric bacterial pathogens. The BD MAX Enteric Bacterial Panel detects nucleic acids from:

- *Salmonella* spp.
- *Campylobacter* spp. (*jejuni* and *coli*)
- *Shigella* spp. / Enteroinvasive *E. coli* (EIEC)
- Shiga toxin 1 (*stx*1) / Shiga toxin 2 (*stx*2) genes (found in Shiga toxin-producing *E. coli* [STEC]) as well as *Shigella dysenteriae*, which can possess a Shiga toxin gene (*stx*) that is identical to the *stx*1 gene of STEC.

Testing is performed on unpreserved soft to diarrheal stool specimens or Cary-Blair preserved stool specimens from symptomatic patients with suspected acute gastroenteritis, enteritis or colitis. The test is performed directly on the specimen, utilizing real-time polymerase chain reaction (PCR) for the amplification of *SpaO*, a *Campylobacter* specific *tuf* gene sequence, *ipaH* and *stx*1/*stx*2. The test utilizes fluorogenic sequence-specific hybridization probes for detection of the amplified DNA.

This test is intended for use, in conjunction with clinical presentation, laboratory findings, and epidemiological information, as an aid in the differential diagnosis of *Salmonella*, *Shigella*/EIEC, *Campylobacter* and Shiga toxin-producing *E. coli* (STEC) infections. Results of this test should not be used as the sole basis for diagnosis, treatment, or other patient management decisions. Positive results do not rule out co-infection with other organisms that are not detected by this test, and may not be the sole or definitive cause of patient illness. Negative results in the setting of clinical illness compatible with gastroenteritis may be due to infection by pathogens that are not detected by this test or non-infectious causes such as ulcerative colitis, irritable bowel syndrome, or Crohn's disease.

Type of Use *(Select one or both, as applicable)*

☒ Prescription Use (Part 21 CFR 801 Subpart D) ☐ Over-The-Counter Use (21 CFR 801 Subpart C)

PLEASE DO NOT WRITE BELOW THIS LINE – CONTINUE ON A SEPARATE PAGE IF NEEDED.

FOR FDA USE ONLY

Concurrence of Center for Devices and Radiological Health (CDRH) *(Signature)*

John Hobson -S
2014.05.06 11:33:07 -04'00'

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